

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hodgson, John
Lawlor, Elizabeth

(ii) TITLE OF THE INVENTION: Novel tRNA Synthetase

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 17-JAN-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 9601095.4
(B) FILING DATE: 19-JAN-1996

(A) APPLICATION NUMBER: 9615845.6
(B) FILING DATE: 27-JUL-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: P31353

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCTAAAG	AAACATTTTA	TATAACAACC	CCAATATACT	ATCCTAGTGG	GAATTTACAT	60
ATAGGACATG	CATATTCTAC	AGTGGCTGGA	GATGTTATTG	CAAGATATAA	GAGAATGCAA	120
GGATATGATG	TTCGTTATTT	GACTGGAACG	GATGAACACG	GTCAAAAAAT	TCAAGAAAAA	180
GCTCAAAAAG	CTGGTAAGAC	AGAAATTGAA	TATTTGGATG	AGATGATTGC	TGGAATTAAA	240
CAATTGTGGG	CTAAGCTTGA	AATTTCAAAT	GATGATTTTA	TCAGAACAAC	TGAAGAACGT	300
CATAAACATG	TCGTTGAGCA	AGTGTTTGAA	CGTTTATTAA	AGCAAGGTGA	TATCTATTTA	360
GGTGAATATG	AAGGTGCGTA	TTCTGTTCCG	GATGAAACAT	ACTATACAGA	GTCACAATTA	420
GTAGACCCAC	AATACGAAAA	CGGTAAAATT	ATTGGTGGCA	AAAGTCCAGA	TTCTGGACAC	480
GAAGTTGAAC	TAGTTAAAGA	AGAAAGTTAT	TTCTTTAATA	TTAGTAAATA	TACAGACCGT	540
TTATTAGAGT	TCTATGACCA	AAATCCAGAT	TTTATACAAC	CACCATCAAG	AAAAAATGAA	600
ATGATTAACA	ACTTCATTAA	ACCAGGACTT	GCTGATTTAG	CTGTTTCTCG	TACATCATTT	660
AACTGGGGTG	TCCATGTTCC	GTCTAATCCA	AAACATGTTG	TTTATGTTTG	GATTGATGCG	720
TTAGTTAACT	ATATTTTCAGC	ATTAGGCTAT	TTATCAGATG	ATGAGTCACT	ATTTAACAAA	780
TACTGGCCAG	CAGATATTCA	TTTAATGGCT	AAGGAAATTG	TGCGATTCCA	CTCAATTATT	840
TGGCCTATTT	TATTGATGGC	ATTAGACTTA	CCGTTACCTA	AAAAAGTCTT	TGCACATGGT	900
TGGATTTTGA	TGAAAGATGG	AAAAATGAGT	AAATCTAAAG	GTAATGTTGT	AGACCCTAAT	960
ATTTTAATTG	ATCGCTATGG	TTTAGATGCT	ACACGTTATT	ATCTAATGCG	TGAATTACCA	1020
TTTGGTTCAG	ATGGCGTATT	TACACCTGAA	GCATTTGTTG	AGCGTACAAA	TTTCGATCTA	1080
GCAAATGACT	TAGGTAACCT	AGTAAACCGT	ACGATTTCTA	TGGTTAATAA	GTACTTTGAT	1140
GGCGAATTAC	CAGCGTATCA	AGGTCCACTT	CATGAATTAG	ATGAAGAAAT	GGAAGCTATG	1200
GCTTTAGAAA	CAGTGAAAAG	CTACACTGAA	AGCATGGAAA	GTTTGCAATT	TTCTGTGGCA	1260
TTATCTACGG	TATGGAAGTT	TATAAGTAGA	ACGAATAAGT	ATATTGACGA	AACAACGCCT	1320
TGGGTATTAG	CTAAGGACGA	TAGCCAAAAA	GATATGTTAG	GCAATGTAAT	GGCTCACTTA	1380
GTTGAAAATA	TTTCGTTATG	AGCTGTATTA	TTACGTCCAT	TCTTAACACA	TGCGCCGAAA	1440
GAGATTTTGT	AACAATTGAA	CATAACAAT	CCTCAATTTA	TGGAATTTAG	TAGTTTAGAG	1500
CAATATGGTG	TGCTTACTGA	GTCAATTATG	GTTACTGGGC	AACCTAAACC	TATTTTCCCA	1560

```

AGATTGGATA GCGAAGCGGA AATTGCATAT ATCAAAGAAT CAATGCAACC GCCTGCTACT 1620
GAAGAGGAAA AAGAAGAGAT TCCTAGCAAA CCTCAAATTG ATATTAAAGA CTTTGATAAA 1680
GTTGAAATTA AGGCAGCAAC GATTATTGAT GCTGAACATG TTAAGAAGTC AGATAAGCTT 1740
TTAAAAATTC AAGTAGACTT AGATTCTGAA CAAAGACAAA TTGTATCAGG AATTGCCAAA 1800
TTCTATACAC CAGATGATAT TATTGGTAAA AAAGTAGCAG TTGTTACTAA CCTGAAACCA 1860
GCTAAATTAA TGGGACAAAA ATCTGAAGGT ATGATATTAT CTGCTGAAAA AGATGGTGTA 1920
TTAACCTTAG TAAGTTTACC AAGTGCAATT CCAAATGGTG CAGTGATTAA ATAA 1974

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Ala Lys Glu Thr Phe Tyr Ile Thr Thr Pro Ile Tyr Tyr Pro Ser
 1             5             10             15
Gly Asn Leu His Ile Gly His Ala Tyr Ser Thr Val Ala Gly Asp Val
      20             25             30
Ile Ala Arg Tyr Lys Arg Met Gln Gly Tyr Asp Val Arg Tyr Leu Thr
      35             40             45
Gly Thr Asp Glu His Gly Gln Lys Ile Gln Glu Lys Ala Gln Lys Ala
      50             55             60
Gly Lys Thr Glu Ile Glu Tyr Leu Asp Glu Met Ile Ala Gly Ile Lys
      65             70             75             80
Gln Leu Trp Ala Lys Leu Glu Ile Ser Asn Asp Asp Phe Ile Arg Thr
      85             90             95
Thr Glu Glu Arg His Lys His Val Val Glu Gln Val Phe Glu Arg Leu
      100            105            110
Leu Lys Gln Gly Asp Ile Tyr Leu Gly Glu Tyr Glu Gly Trp Tyr Ser
      115            120            125
Val Pro Asp Glu Thr Tyr Tyr Thr Glu Ser Gln Leu Val Asp Pro Gln
      130            135            140
Tyr Glu Asn Gly Lys Ile Ile Gly Gly Lys Ser Pro Asp Ser Gly His
      145            150            155            160
Glu Val Glu Leu Val Lys Glu Glu Ser Tyr Phe Phe Asn Ile Ser Lys
      165            170            175
Tyr Thr Asp Arg Leu Leu Glu Phe Tyr Asp Gln Asn Pro Asp Phe Ile
      180            185            190

```

Gln Pro Pro Ser Arg Lys Asn Glu Met Ile Asn Asn Phe Ile Lys Pro
 195 200 205
 Gly Leu Ala Asp Leu Ala Val Ser Arg Thr Ser Phe Asn Trp Gly Val
 210 215 220
 His Val Pro Ser Asn Pro Lys His Val Val Tyr Val Trp Ile Asp Ala
 225 230 235 240
 Leu Val Asn Tyr Ile Ser Ala Leu Gly Tyr Leu Ser Asp Asp Glu Ser
 245 250 255
 Leu Phe Asn Lys Tyr Trp Pro Ala Asp Ile His Leu Met Ala Lys Glu
 260 265 270
 Ile Val Arg Phe His Ser Ile Ile Trp Pro Ile Leu Leu Met Ala Leu
 275 280 285
 Asp Leu Pro Leu Pro Lys Lys Val Phe Ala His Gly Trp Ile Leu Met
 290 295 300
 Lys Asp Gly Lys Met Ser Lys Ser Lys Gly Asn Val Val Asp Pro Asn
 305 310 315 320
 Ile Leu Ile Asp Arg Tyr Gly Leu Asp Ala Thr Arg Tyr Tyr Leu Met
 325 330 335
 Arg Glu Leu Pro Phe Gly Ser Asp Gly Val Phe Thr Pro Glu Ala Phe
 340 345 350
 Val Glu Arg Thr Asn Phe Asp Leu Ala Asn Asp Leu Gly Asn Leu Val
 355 360 365
 Asn Arg Thr Ile Ser Met Val Asn Lys Tyr Phe Asp Gly Glu Leu Pro
 370 375 380
 Ala Tyr Gln Gly Pro Leu His Glu Leu Asp Glu Glu Met Glu Ala Met
 385 390 395 400
 Ala Leu Glu Thr Val Lys Ser Tyr Thr Glu Ser Met Glu Ser Leu Gln
 405 410 415
 Phe Ser Val Ala Leu Ser Thr Val Trp Lys Phe Ile Ser Arg Thr Asn
 420 425 430
 Lys Tyr Ile Asp Glu Thr Thr Pro Trp Val Leu Ala Lys Asp Asp Ser
 435 440 445
 Gln Lys Asp Met Leu Gly Asn Val Met Ala His Leu Val Glu Asn Ile
 450 455 460
 Arg Tyr Ala Ala Val Leu Leu Arg Pro Phe Leu Thr His Ala Pro Lys
 465 470 475 480
 Glu Ile Phe Glu Gln Leu Asn Ile Asn Asn Pro Gln Phe Met Glu Phe
 485 490 495
 Ser Ser Leu Glu Gln Tyr Gly Val Leu Thr Glu Ser Ile Met Val Thr
 500 505 510
 Gly Gln Pro Lys Pro Ile Phe Pro Arg Leu Asp Ser Glu Ala Glu Ile
 515 520 525
 Ala Tyr Ile Lys Glu Ser Met Gln Pro Pro Ala Thr Glu Glu Glu Lys
 530 535 540

37